



Db	8658	CAAGCAATCCACCTGAGCTCCAAAATGCTGGGACCCAGCCCTACGC	8717	Qy	92	-----	Qy	92	-----
Qy	92	-----	Db	9798	CCCTGGCCCTGGAGGTGCCACAGCCCTCCATCGGCCTCACCTACCGAC	9857	Db	9798	CCCTGGCCCTGGAGGTGCCACAGCCCTCCATCGGCCTCACCTACCGAC
Db	8718	TAAGAATTGAATGAGGGCTAATTTCATTAAGATGCTGGTACACAAAGCATATA	8777	Qy	92	-----	Qy	92	-----
Qy	92	-----	Db	9858	AAAGTACACATCACCTGGCAGCTAACACAAGCTGATGTTCTCACAGTCTGGGGCT	9917	Db	9858	AAAGTACACATCACCTGGCAGCTAACACAAGCTGATGTTCTCACAGTCTGGGGCT
Db	8778	TTCCTTAATCCAAAGCAATTCAACAGTCTGAATCCCTAACAGCCCTTGTAAAGATG	8837	Qy	92	-----	Qy	92	-----
Qy	92	-----	Db	9918	GGAGGCCAAGATTGGGTACGAGGGTGGTCTCTGCTGAGGCTCTGCTGGCT	9977	Db	9918	GGAGGCCAAGATTGGGTACGAGGGTGGTCTCTGCTGAGGCTCTGCTGGCT
Db	8838	CCTGGCCCAGCGGGTGGCTCACGGCCCTGTAACTCCAGCACTTGGAAAGGCCAAGGGGG	8897	Qy	92	-----	Qy	92	-----
Qy	92	-----	Db	9978	GCCCGTGGCCATCTCTCCCTGCGTCTTCCCTGTCATGTTGCTCTGATGCCCT	10037	Db	9978	GCCCGTGGCCATCTCTCCCTGCGTCTTCCCTGTCATGTTGCTCTGATGCCCT
Db	8898	CGGATCACCTGAGGTCCGGAGTTCGAGACAGCAGCTGGOCACATGGAGAACCCCGTCTC	8957	Qy	92	-----	Qy	92	-----
Qy	92	-----	Db	10038	TTCCTAACAGGACATAAGTCATATCGGATGAGGGCCACCCCTGTCAGTCCT	10097	Db	10038	TTCCTAACAGGACATAAGTCATATCGGATGAGGGCCACCCCTGTCAGTCCT
Db	8958	TACTAAAAATACAAAAATCAGCTGGCTGGATGGCTGAGCTGTAATCGAACCTACTCTGG	9017	Qy	92	-----	Qy	92	-----
Qy	92	-----	Db	10098	TATAATGACCCCTTATTATTATTGAGATGGAGTCCTCCCTGTCACCCAAGCTGGAG	10157	Db	10098	TATAATGACCCCTTATTATTATTGAGATGGAGTCCTCCCTGTCACCCAAGCTGGAG
Db	9018	GGGCTGGGGAAAGAGAAATGCCCTGGAAACCCGGGAGGGGGTGCAGTGAGCTAAGATG	9077	Qy	92	-----	Qy	92	-----
Qy	92	-----	Db	10158	TGAGTGGCGGAGCCCTCTGCTCACTGCAACCTCTGCTCCCGGGTTCAACTGTCCT	10217	Db	10158	TGAGTGGCGGAGCCCTCTGCTCACTGCAACCTCTGCTCCCGGGTTCAACTGTCCT
Db	9078	CACCATTGCACTCATCCCTGGAAACAAGAGTGAACCTCCGTCAGTGGTACCTGACTACACCCAGCTAATTTC	9137	Qy	92	-----	Qy	92	-----
Qy	92	-----	Db	10218	GCCTCACCCCTCTGAGTAGCTGGATTACAGGTACCTGACTACACCCAGCTAATTTC	10277	Db	10218	GCCTCACCCCTCTGAGTAGCTGGATTACAGGTACCTGACTACACCCAGCTAATTTC
Db	9138	AACAAACCACTGGCGCTTGGCTCAGCGCTTAATCCAGGACTCTTGGAGGCCAGG	9197	Qy	92	-----	Qy	92	-----
Qy	92	-----	Db	10278	GTATTTTAGTAGAGACGGGGTTTACACATGTTGCCAGGGTGGCTCGAACCTCTGACC	10337	Db	10278	GTATTTTAGTAGAGACGGGGTTTACACATGTTGCCAGGGTGGCTCGAACCTCTGACC
Db	9198	TGGCGGATCCCTTGGAGTTCAAGACCAAGCTGATCAACATGGAGAACCCCTG	9257	Qy	92	-----	Qy	92	-----
Qy	92	-----	Db	10338	TCAGGTGATCCACCTGGCCCTCTGAAAGTGGCTCGAACCTGGATGAGCCAC	10397	Db	10338	TCAGGTGATCCACCTGGCCCTCTGAAAGTGGCTCGAACCTGGATGAGCCAC
Db	9258	TCTCTACTAAAAATGCAAAATTAGCTGACCGTGGTAGCCGGCCCTGTAATCCAGCTA	9317	Qy	92	-----	Qy	92	-----
Qy	92	-----	Db	10398	GCCAGGGCATTAATGTTAACCCATCTAACAAAGACCCATCACATTCTGAGGT	10457	Db	10398	GCCAGGGCATTAATGTTAACCCATCTAACAAAGACCCATCACATTCTGAGGT
Db	9318	CTCGGAGGGTGAAGGGAGATAAGCTTGGAGGTGGCTGAGTGGAGCA	9377	Qy	92	-----	Qy	92	-----
Qy	92	-----	Db	10458	CCTGGGGTTAGGGCTTCTAGATGCGGCTGGATGGGGTCAAGTTCAGCTGGCTACAGTC	10517	Db	10458	CCTGGGGTTAGGGCTTCTAGATGCGGCTGGATGGGGTCAAGTTCAGCTGGCTACAGTC
Db	9378	AGATGTGCGTTGACTCAGCGTGGTACAGAGGAAACTCCGTCATAAACACACA	9437	Qy	92	-----	Qy	92	-----
Qy	92	-----	Db	10518	ACCAAGCCCTGGCTTCTGGATTCCTGGATGGGGTCAAGCTGGCTACAGCTGG	10577	Db	10518	ACCAAGCCCTGGCTTCTGGATTCCTGGATGGGGTCAAGCTGGCTACAGCTGG
Db	9438	ACAAACACAAACAAACCCCTGACCCAGAGGACAGAAATCCCATCACCTGAGGTTCTCA	9497	Qy	92	-----	Qy	92	-----
Qy	92	-----	Db	10578	CTCCCGCTGAGTGGCCCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG	10637	Db	10578	CTCCCGCTGAGTGGCCCTGGCTGGCTGGCTGGCTGGCTGGCTGG
Db	9498	GAAGACTATCTCTCGTGAAGGAGTCATCCAAGCTGGCATTTCACTGGGAAACT	9557	Qy	92	-----	Qy	92	-----
Qy	92	-----	Db	10638	GAAGGCTCTCCAGGAGACTCTGGCTGGGGCTGGCTGGCTGGCTGGCTGG	10697	Db	10638	GAAGGCTCTCCAGGAGACTCTGGCTGGGGCTGGCTGGCTGGCTGGCTGG
Db	9558	GACACCTGGACTGGCCAGCTCCACAGAGCCCTGGCTGGCTGGCTGGCTGG	9617	Qy	92	-----	Qy	92	-----
Qy	92	-----	Db	10758	CGGACTGCGAGATTCTGGAGGATGGGGCTGGCTGGCTGGCTGGCTGG	10817	Db	10758	CGGACTGCGAGATTCTGGAGGATGGGGCTGGCTGGCTGGCTGGCTGG
Db	9618	GTGCCAGCCTCAGGCAAGAGTGAAGTCAAGGCTTGTGTCCTTGAAGAGTGT	9677	Qy	92	-----	Qy	92	-----
Qy	92	-----	Db	10818	GCAGCCAGGGCTCTGGAGCACCCAGCACGGTGTGGCTGGAGGAGGAG	10877	Db	10818	GCAGCCAGGGCTCTGGAGCACCCAGCACGGTGTGGCTGGAGGAGGAG
Db	9678	GGGCTCAGAGGAGGAGAAGGGCCCATGGAAACAGCRAACCCGGATGAGGCTTAAGGCTGGTGAAGGAA	9737	Qy	92	-----	Qy	92	-----
Qy	92	-----	Db	9738	GGGGCTCAGAGGAGGAGAAGGGAGAAGGGCCCATGGATCGCTGATCAAGGGCATCAAACCCCTGG	9797	Db	9738	GGGGCTCAGAGGAGGAGAAGGGAGAAGGGAGAAGGGCCCATGGATCGCTGATCAAGGGCATCAAACCCCTGG



Db	13038	GTGGAGCAGGGGACCCCTCCGGGGCCCTGTGCTGGCTGTGGCTCAT 13097	-----	305
Qy	306	-----	-----	-----
Db	13098	CTGAGGATTCGGACCCCTGGAGATGACCCCTCCGTTCCGTCATTCTCTGGCGT 13157	-----	305
Qy	306	-----	-----	-----
Db	13158	CGTGTGGTTCCCTCTTCTTCTTAAGTGAAGCTAAAGGAGCG 13217	-----	305
Qy	306	-----	-----	-----
Db	13218	CCTGTGAAGGCGAGTAGATCCCTCTCGGTACCCCTGGCTGTGGCGCC 13277	-----	305
Qy	306	-----	-----	-----
Db	13278	AGCCCCCACGCCGCCCTGCATCCCCCTGCAGCGTGTAGCACGTGAGCTCCCTCAAGCT 13337	-----	305
Qy	306	-----	-----	-----
Db	13338	CCTGCGGCACTGTGGACAGCCGGTTCAACAAATGCCCAATTGTGGAGTTCACGT 13397	-----	305
Qy	306	-----	-----	-----
Db	13398	TTTCCTTTGTTTTGTTCTAAACAAATGCCAACGGGAAACCTCCAGGGCCAG 13457	-----	305
Qy	306	-----	-----	-----
Db	13458	TGGTCGAGACAAGGATAGTTTAAATGCAGGATAGTGTCTTTCTTTCTTCT 13517	-----	305
Qy	306	-----	-----	-----
Db	13518	TTTTTTTTGAGACGGGGCTCGCTCTGTCGCCAGGTGTGGAGTCAGTGGCGA 13577	-----	305
Qy	306	-----	-----	-----
Db	13578	TCTCGGCTCACTGCATGCTCGCTTCTGGCTCAGCTCTAAAGTAGCTG 13637	-----	305
Qy	306	-----	-----	-----
Db	13638	GGACTACAGGTGCCGCCACACGCCGCTTAATTTTGTATTTTTATTAGAGAG 13697	-----	305
Qy	306	-----	-----	-----
Db	13698	ATGGGGTTTCACCGTGTGGCAGGGATGGTCTCGATCTCCCTGACCTCGTGTGACCCAC 13755	-----	305
Qy	306	-----	-----	-----
Db	13758	CTGGCCCTCCAAAAGTGTGGGATTAAAGGGTGTAGGGCACCACGCCGGCTAATGCCAGGA 13817	-----	305
Qy	306	-----	-----	-----
Db	13818	TAGTTCTAATGGAGGGAACCTGAGACATGGCAGGGCCGTCCAAACACGGCTCTGTGCTGG 1387	-----	305
Qy	306	-----	-----	-----
Db	13878	CGGGCAGGGGACCTGGCCATTCTGCCGGGAGCCGACTCTGTAGCCGTGACCC 1393	-----	305
Qy	306	-----	-----	-----
Db	13998	GAGCGGAACCGTGGGGAAATGAGAAGCCACAGGGATGGAGGAGGGAGGG 1405	-----	305
Qy	306	-----	-----	-----
Db	14058	CAAGGAGATCTGAGAGGGTTCTGGGGCTGCGCACTGGTATSTGGACCCAGATCTAG 1411	-----	305
Qy	306	-----	-----	-----
Db	14118	TAAACCGAGAGGTCTGGGTAGACCTGCGCTACTCGCCCTGTAGGCCAACGGCTCA 1411	-----	305





Qy	810	-	809	Db	20718	CCAGGCCGGCGTTTACTTCACCTCAGGGACCCCTCCACCCAG	20777
Db	19638	GGGAGGACTGTGAGCCCTCACAGGCTGTCTGACCCCCACTTGGGACCCCTCTCCACCCAG	19697	Qy	810	-	809
Qy	810	-	809	Db	20778	AGAACGCTGGAAAAGCTGCTGGTACACACAGCTGGATCAGCCCCTGGTGGACCC	20837
Db	19698	GGCTTTCGGGAACCCGTGACTCCACCCACACAGCTGGATCAGGGCT	19757	Qy	810	-	809
Qy	810	-	809	Db	20838	CTCACAGAGAGCCGGAAAGCTCTGGTACACAGCTGGATCAGCCAGGGCTGGT	20897
Db	19758	CATCAGGGACGTGCAATTCAATCACGAAACAGTCCCATCTTCCTGTGTCAGGCAGAATG	19817	Qy	810	-	809
Qy	810	-	809	Db	20898	GCGCACCCCTGGACTCCGGCCAGGAAGGACACGGAGGGCATGGCTGGCGGCCG	20957
Db	19818	CGCGGGTGGACCTCGCTCGAGGCCAACCCCTGATGCTGTCACACCAGGGAC	19877	Qy	810	-	809
Qy	810	-	809	Db	20938	GGTGGGGCTCAGCCATTGGTACACAGGGCTGATCATCTGGAAAGGGTAGTAGT	21017
Db	19878	ACCTCTGGGATGCGCACTGGGAGCTGGGGAGACTGGGG	19937	Qy	810	-	809
Qy	810	-	809	Db	21018	GCGACTGGCGGTGACCCCTCCGGTACCGGATCAGCCATCACCCTCCGGAGC	21077
Db	19938	GGGGTGGGGAGAGGGCACCCAGCGGGCTATGACGGGCCAGGTGGGATGGGGAGACTGGGG	19997	Qy	810	-	809
Qy	810	-	809	Db	21078	CGGCCCTCAGCAGCGGGCACCTGGGTCTCTGGTGGGGATGGCACCGAGTCACCTCT	21137
Db	19998	GGGGTGGGAGAGGGGTGACCCAGGGAAACAGCAGCCCTGGCCAGAGTCAGACCA	20057	Qy	810	-	809
Qy	810	-	809	Db	21138	GAGGGCATGGGGTACAGTCACCGTCACTGGGCCACCCCTCATGAAAGTGT	21197
Db	20058	GAAGCGGGCTCTCTCAAGGGCAAGAGGGTCAAGGAGCCGGCCAG	20117	Qy	810	-	809
Qy	810	-	809	Db	21198	TGGCAAAGGCCGGGTGGGGCTGZAGCTCCGTGGCAGCCTGGAGGCC	21257
Db	20118	GAAGATGGGGGTGACACATGTGGATGAGGGCAAAGTGGAGGCAATGGGTGAC	20177	Qy	810	-	809
Qy	810	-	809	Db	21258	GCCCCAGGTGAAACGGGAATCTCCAGCTGGGGCAGCAGCTCCGGCTGT	21317
Db	20178	CAGCTGGGACAAGGGCACAGACAGGAGGACCCGGATGTCTGGGCTGGCAGGTG	20237	Qy	810	-	809
Qy	810	-	809	Db	21318	TGGANCCCAGCCCCAACACTCGAGCCACCCGGGCACTACTCCACAGT	21377
Db	20238	GGCTGCCCTGCAATGGGCCAGCAGGGCTGGCTGGCAGGTGG	20297	Qy	810	-	809
Qy	810	-	809	Db	21438	TCCCATTTGGAAAGAAAAGCTGCCCCAGGGCACCCAGGGCTCACAACA	21497
Db	20298	AAATGGGGCTGGGAAACGGGGCTGTCAAGCAGGGCACTGGGGAGGGAG	20357	Qy	810	-	809
Qy	810	-	809	Db	21448	GCAGCCCCAGGGCAACACATAAGGCCCTTCTCAGATAGCCGGCAGAGGG	21557
Db	20358	GGGAGCTCAGGGTGTGCTGGGGAGGAAAGTGGTTCTGGCTGGGGCAAG	20417	Qy	810	-	809
Qy	810	-	809	Db	21558	AACAGCGAGACAAGGACTGCTGAACCAAGACACAGGCACTGGAGGGA	21617
Db	20418	ATCCCTTGTCCCCACACCCCCGGCGTGGCTGGACCCCTGAGCTGACCTAGT	20477	Qy	810	-	809
Qy	810	-	809	Db	21618	GGGAAACAGCAGGGCTTAGCTGAACACAGGGCACTGGGAGCCATGGAGT	21677
Db	20478	TACCCCTTCCCCGTACCCCACTGCAAAAGGGTAAGGTGGCTTACATGTGAGAAGGACAT	20537	Qy	810	-	809
Qy	810	-	809	Db	21678	AGCTGTGAGGACTTTGATTTCACATTTTGTGAGTGGAGT	21737
Db	20538	GGGGCCATCAGCTGGAGATGCTGCTATGGCAAGCAGTGGGGAGTCCATGGATGGGG	20657	Qy	810	-	809
Qy	810	-	809	Db	21738	GGCTGTGGCCAGGGTGGAGTACACGGTGGCAATCTGGCTCACAGCAACCTGGCT	21797
Db	20658	GGAGGTGAGGGAGAGCCCTGGAGTAACAGTCGACGCCACTGGCCAAAC	20717	Qy	810	-	809
Qy	810	-	809	Db	21798	GGCTGTGGCCAGGGTGGAGTACACGGTGGCAATCTGGCTCACAGCAACCTGGCT	21897

Db	21798	CATGTTCAAGTGAATTCTAGCCCTCATGCCCTAGCCCTCCGAGTAGCTGGATTACAGGGGCCCGC 21857	QY	810	-
QY	810	-	Db	22938	TGAGAACCCGAGATCGCCTCCAGGGCCCTCCAGCTGGCATGCCATCCGGTGCCTCC 22997
Db	21858	CAACACGCTGGCTAACTTTGTATTAGATGGATTCTGCCATTGCGCAG 21917	QY	810	-
QY	810	-	Db	22958	GCCATCCACAGCCAGGGCACACCCACATGGCTCTGTCGCCACATCAGAGG 23057
Db	21918	GCTAGGCTAACACTCTGGCTCAAGTGTATCCACCCGCCCTGCCAGTGGGG 21977	QY	810	-
QY	810	-	Db	23058	GACCCACACAAAGGAGGGCTGCATGGAGCTGGGAGGCCACCCGTGATACTG 23117
Db	21978	ATCACAGGCTGAGCCACCCAGCCAGCTGATTCCATTTCATTTAAATTTCCTTC 22037	QY	810	-
QY	810	-	Db	23118	CCCCTCACCCCTACCATCAAGTACCCGAGGGTGGGTGCCACATCCTCCACA 23177
Db	22038	TTTCCTCTCTCTCTCTGAGACAGGGTCTGGCTCTGGACTGGAGT 22097	QY	810	-
QY	810	-	Db	23178	GGCCTTTCAAGGGATGACTCTGAGAGGGAAAGAAAAGAGGGACACGGTAGAGAG 23237
Db	22098	GGAGTGGTTCGATCTGGCTCACTGAACTCTCCCTGGCCCAAGCATCCCTCA 22157	QY	810	-
QY	810	-	Db	23238	GTCCCCAGGATCTCCCACTGAGAANGGGAGCCGGCAGGGGACTCCGAGAGAG 23297
Db	22158	CCTCAGCCTCCAACTGAGCTGGAGTACAGCACAGCCACACGCCAACGTA 22217	QY	810	-
QY	810	-	Db	23298	ACCACTCTCCACCTCTGACAGCCCAAGCCCCAGGAACTGCCCTCAC 23357
Db	22218	GTATTTTTTTAGAAGATGAGGTCTGTCTGTAGCCPAGGCTGGCTCTGA 22277	QY	810	-
QY	810	-	Db	23358	CCAAAGGAGTGGGGCTCTGGGAGAGGGCACCTGTTGTC 23417
Db	22278	CTTAGGGCTAACCAATCTGCCAACCTGGCTTCCACAGCTGGATAATAGCTG 22337	QY	810	-
QY	810	-	Db	23418	GGGCCAGTCGGAGGCCCTGGAAAGAACCCGCTCATGATCCATGCTCA 23477
Db	22338	CCACTGCTCTGGCAGCCACTGGCCAGGCCAAAGGACTTTCAATGAAACACCA 22397	QY	810	-
QY	810	-	Db	23458	TGATGGGGCTCCCTGACCTTGTGCTGGCATGCCAAAGCCACCTCCAGG 23537
Db	22398	CAGTCAGCCACCCAGGGTCAGGAAGGGACCCCTCCCAAGGTACCAAGGTGGCTCAG 22457	QY	810	-
QY	810	-	Db	23538	ACCCGGCCCTGGCAAGACAGGGCGCTGGCATCACTAGGTGGGGCTTAGGG 23597
Db	22458	CAGCCCTTCCACCCATCCAGGTACTCTGGAGAACCTGGGAACCTCAGGT 22517	QY	810	-
QY	810	-	Db	23568	GGAGGGCTGGGTGGCTGCCCTGGAGGGGACTGGCTGGAGGAGGGCT 23657
Db	22518	GGGGCACCTAACATGATGATGTTGACTCTGGACTCTGGATCACTGGCTCC 22577	QY	810	-
QY	810	-	Db	23598	GCTGGAGGGAGGGGGCTGGCCAAATGGTGGGGAGGTGCTGGAGGGGG 23777
Db	22538	GTGCAAGGGAGTGGSCACAGTGGCTAGGGAGGGGGCTGGGGAGGGCT 22697	QY	810	-
QY	810	-	Db	23718	GCCTGGAGGGAGGGGGCTGGCTGGGGAGGTGCTGGAGGGGG 23897
Db	22578	AGGTGAGGTGCACTGAGGTGGAGGCCCTCCGCTTCAAGAGGAAAGGGTGTCT 22637	QY	810	-
QY	810	-	Db	23778	CAGGCTGGAGGGCTGCCAGGGGGCTGGCTGGAGGGGGCTGGAGAGAG 23837
Db	22698	CGAGGGCCTCCGCATCCAGCAACTCAGAGAGAACCTTGATGAAGTGA 22757	QY	810	-
QY	810	-	Db	23838	GGGGTCAGACAGCCAGGGCTGGGGAGGGGGCTGGCTGGAGGG 23897
Db	22758	TGTTGCGAGGCTCCTCCAGAGTGGTACAGGATCCCTGACCGAGAAC 22817	QY	810	-
QY	810	-	Db	23898	TGAGCTGGGTCTGCTGTGAGGAGGGGCTGGCTGAACGGCTATGCTGAGTCACA 23957
Db	22818	AGAGGCCAACGGCGCTGAGGGGGCTCACCCAGCCTCACCGGGCTCATCC 22877	QY	810	-
QY	810	-	Db	23958	TTTGCCACGGACGGAGGGCTGGAGACGGGGGGACCCCTGGCCAGCATGGACAGGGGGAAACACAGT 24017

Qy	810	- - - - -	809
Db	24018	AGTCCCTGAGGGAACAGGTGGCCCTGGCCAGGGCAGAGGATGACCCAG	2407
Qy	810	- - - - -	809
Db	24078	GGAGCCGAAGGCCCTTGGGCCAGGGCTGTGGGAGGAGACCTTGACTT	2413
Qy	810	- - - - -	809
Db	24138	TGAGCCCAGCCACGTGGTGTCCGGGTCCTATCTCGGGTTAGTTCTC	2419
Qy	810	- - - - -	809
Db	24198	TCCCCCTCCCTATCCGAAGTGGATTGCAAGAGTGGCAAGACCTGGACTTG	2425
Qy	810	- - - - -	809
Db	24248	AGACATCTGGAGGGAAAGACAGTGGTCCCAGTGGCCACACATGGCCCCGGTCAA	24317
Qy	810	- - - - -	809
Db	24318	TCCTGATTGGCACTGGACACTGGACGTGCCATTTCAGGGGGAAACACTGAGGCCGA	24377
Qy	810	- - - - -	809
Db	24378	CCCCCTGGACGGGGCTGTGGGGCAGGGAGTCCCTAGCAGCCCTAGCTCTGA	24437
Qy	810	- - - - -	809
Db	24438	CGCAGGGAGGCCAGGGCACCCGGGACAGCTGTCTCCCTGAGCTCAGCTTCAGGAGT	24497
Qy	810	- - - - -	809
Db	24498	GCTATTCCTAGCGGGGAGTGGGGCTGCTCCAGGGAGAAGGGAGCCCTCTC	24557
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Db	24558	CCTGGCACGACCCCTTCCTCCGACCTCAGACAGGGAGCTGGGACCCGGCTCACCCAG	24617
Qy	810	- - - - -	809
Db	24618	TTTCACCCAGSTCTGACGTTGAGGTCCOCATCTGGAGCGGGGCCCTCAC	24677
Qy	810	- - - - -	809
Db	24678	GGAGAGGAAGTTCTGGTACTTAGGGGTGCCATAACCTGTGGGGCCCACGCCCTGCGC	24737
Qy	810	- - - - -	809
Db	24738	ACCTCCCGTGAAGGCCCTCGCTGTGCCCTCACCTGCAAGCCCACTTCCAGAGTCCCGGGCTGCGCCGGCTC	24857
Qy	810	- - - - -	809
Db	24858	AGTTTCCCCCTGGCCCCCGGGGGTGGTGCAGGGCTGGCTACCTTGAGGAAG	24977
Qy	810	- - - - -	809
Db	24978	GATGGCCAGGTGGTGTGGCAATAGGGTCTCCAGGGTCCATACGGCTTGCCAG	24917
Qy	810	- - - - -	809
Db	24918	GGCGGGGCCAGGGTGTGGTGTGGCTAGGGGTCTCCAGGGTCCATACGGCTTGCCAG	25037
Qy	810	- - - - -	809
Db	25038	GCAGTTCTCGCCGGGGAAAGATGGGGTCCGCTGGGGCGCTCATGTCAGGCTGG	25097
Qy	810	- - - - -	809

TUES MAR 5 15:12:34 2002

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Sequence ac005329: residues 1 to 32760
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  ; DEFINITION Homo sapiens chromosome 19, cosmid R34382, complete sequence.
  ; VERSION    AC005329.1   GI:3342732
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  ; ORGANISM  Homo sapiens
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  ;          Best Local Similarity 1.9%; Pred No. 0; Mismatches 3.37; Indels 24/29; Gaps 19
  ;          Matches 487; Conservative 487; Gaps 0
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  QY 70  -----69
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  QY 70  -----69
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  QY 70  -----69
  Db 28740 CAGGCAGGGTGGCTACGGCTGTAACTCCAGCACTTGGAGGCCAAGTGGGGGTCA 28561
  QY 70  -----69
  Db 28620 ATATCAAATAATAGCAGGGCTGGGTGGGGTGTGTAAATCCAGTACTCAGGGGCT 28501
  QY 70  -----69
  Db 28560 GAGGGAGGAGTCGCTGAAACCCGGAGGGAGAGTTGTAGCGAGCCAGATCACACCA 2850
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